
Sequence Listing was accepted.

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Reviewer: Anne Corrigan

Timestamp: [year=2011; month=3; day=9; hr=10; min=5; sec=19; ms=155;]

Validated By CRFValidator v 1.0.3

Application No: 10569000 Version No: 4.0

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Finished: 2011-03-01 18:47:45.877

Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 403 ms

Total Warnings: 1

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No. of SeqIDs Defined: 44

Actual SeqID Count: 44

Error code Error Description

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Asp Ser Thr Tyr Leu Asn Pro Gln Ala His Asp Ser Val Leu Gly Ile 35 40 45

Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys Lys 50 55 60

Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile Asp 65 70 75 80

Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr Val 85 90 95

Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg Ala
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Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu Val 115 120 125

Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly Thr
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Glu	Lys	Phe	Ile 180	Gln	Ala	His	Arg	Glu 185	Thr	Asn	Ala	Asp	Ile 190	Thr	Val
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Lys	Ile 210	Asp	Glu	Glu	Gly	Arg 215	Ile	Ile	Glu	Phe	Ala 220	Glu	Lys	Pro	Lys
Gly 225	Glu	Gln	Leu	Lys	Ala 230	Met	Met	Val	Asp	Thr 235	Thr	Ile	Leu	Gly	Leu 240
Asp	Asp	Val	Arg	Ala 245	Lys	Glu	Met	Pro	Tyr 250	Ile	Ala	Ser	Met	Gly 255	Ile
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Ile 385	Glu	Asp	Ser	Leu	Leu 390	Met	Gly	Ala	Asp	Tyr 395	Tyr	Glu	Thr	Glu	Ala 400
Asp	Lys	Lys	Leu	Leu 405	Ala	Glu	Lys	Gly	Gly 410	Ile	Pro	Ile	Gly	Ile 415	Gly
Lys	Asn	Ser	Cys 420	Ile	Arg	Arg	Ala	Ile 425	Ile	Asp	Lys	Asn	Ala 430	Arg	Ile
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Asp Ser Thr Cys Leu Asn Pro Gln Ala His Asp Ser Val Leu Gly Ile 35 40 45

Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys Lys 50 55 60

Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile Asp 65 70 75 80

Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr Val 85 90 95

Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg Ala
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Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu Val 115 120 125

Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly Thr
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Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn Val 145 150 155 160

Met Glu Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp Tyr 165 170 175

Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr Val 180 185 190

Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu Met 195 200 205

Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro Lys 210 215 220

Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu Gly Leu

225 230 235 240

Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly Ile 245 250 255

Tyr Val Phe Ser Lys Asp Val Met Leu Gln Leu Leu Arg Glu Gln Phe 260 265 270

Pro Glu Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala Thr Ser 275 280 285

Ile Gly Lys Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu Asp 290 295 300

Ile Gly Thr Ile Ala Ala Phe Tyr Asn Ala Asn Leu Gly Ile Thr Lys 305 310 315 320

Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Phe Ala Pro Ile Tyr 325 330 335

Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp Val 340 345 350

Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys Ile 355 360 365

Asn His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala Ile $370 \hspace{1cm} 375 \hspace{1cm} 380$

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Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg Ile 420 425 430

Gly Asp Asn Val Lys Ile Leu Asn Ala Asp Asn Val Gln Glu Ala Ala
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225	_		Val		230					235					240
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305	-	1	_	-	310		-	4 -		315			1	-	320

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- Gly Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg $\,420\,$